**CLAIMS:**

1. An isolated or recombinant nucleic acid molecule comprising:
(a) a nucleotide sequence as shown in SEQ ID No.1;
(b) a nucleotide sequence which is the complement of SEQ ID No.1;
(c) a nucleotide sequence which is degenerate with SEQ ID No.1;
(d) a nucleotide sequence hybridising under conditions of high stringency to (a), (b) or (c) or to a hybridisation probe derived from SEQ ID No.1 or the complement thereof;
(e) a nucleotide sequence having at least 80% sequence identity with SEQ ID No.1;
(f) a fragment of (a), (b), (c), (d) or (e) above which is at least 10 nucleotides in length.

2. A nucleic acid according to claim 1 which encodes a polypeptide encoded by an open reading frame of a borrelidin biosynthetic gene cluster, or a domain thereof, wherein said polypeptide has an amino acid sequence selected from the group consisting of SEQ ID Nos.2 to 43 and 113, or at least 80% identity thereto.

3. A nucleic acid according to claim 1 or claim 2 comprising a sequence that encodes a PKS domain selected from AT0 and ACP0, said domains being described by, respectively, amino acids 322-664 and 694-763 of SEQ ID No.2.

4. A nucleic acid according to claim 3 comprising a sequence selected from the group consisting of bases 17147-18175 and 18263-18472 of SEQ ID No.1;

5. A nucleic acid according to claim 1 or claim 2 comprising a sequence that encodes a PKS domain selected from KS1, AT1, KR1 and ACP1, said domains being described by, respectively, amino acids 34-459, 557-885, 1136-1379 and 1419-1486 of SEQ ID No.3.

6. A nucleic acid according to claim 5 comprising a sequence selected from the group consisting of bases 18974-20251, 20543-21529, 22280-23011 and 23129-23332 of SEQ ID No.1;

7. A nucleic acid according to claim 1 or claim 2 comprising a sequence that encodes a PKS domain selected from KS2, AT2, DH2, KR2, ACP2, KS3, AT3, DH3, KR3 and ACP3, said domains being described by, respectively, amino acids 34-459, 559-887, 903-1050, 1354-1597, 1628-1694, 1724-2149, 2245-2576, 2593-2734, 3060-3307 and 3340-3406 of SEQ ID No.4.

8. A nucleic acid according to claim 7 comprising a sequence selected from the group consisting of bases 23785-25062, 25360-26346, 26392-26835, 27745-28476, 28567-28767, 28855-30132, 30418-31413, 31462-31887, 32863-33606 and 33703-33903 of SEQ ID No.1;

9. A nucleic acid according to claim 1 or claim 2 comprising a sequence that encodes a PKS domain selected from KS4, AT4, KR4 and ACP4, said domains being described by, respectively, amino acids 34-459, 555-886, 1179-1423 and 1459-1525 of SEQ ID No.5.

10. A nucleic acid according to claim 9 comprising a sequence selected from the group consisting of bases 34284-35561, 35847-36842, 37719-38453 and 38559-38759 of SEQ ID No.1;

11. A nucleic acid according to claim 1 or claim 2 comprising a sequence that encodes a PKS domain selected from KS5, AT5, DH5, ER5, KR5 and ACP5, said domains being described by, respectively, amino acids 34-457, 553-888, 905-1046, 1401-1690, 1696-1942 and 1975-2041 of SEQ ID No.6.

12. A nucleic acid according to claim 11 comprising a sequence selected from the group consisting of bases 39221-40492, 40778-41785, 41834-42259, 43322-44191, 44207-44947 and 45044-45244 of SEQ ID No.1;

13. A nucleic acid according to claim 1 or claim 2 comprising a sequence that encodes a PKS domain selected from KS6, AT6, KR6, ACP6 and TE, said domains being described by, respectively, amino acids 37-457, 555-883, 1101-1335, 1371-1437 and 1461-1708 of SEQ ID No.7.

14. A nucleic acid according to claim 13 comprising a sequence selected from the group consisting of bases 45622-46884, 47176-48162, 48814-49518, 49624-49824 and 49894-50637 of SEQ ID No.1.

15. A nucleic acid according to any one of the preceding claims comprising a sequence that encodes a PKS module, said module being selected from the group consisting of amino acids 322-763 of SEQ ID No.2, 34-1486 of SEQ ID No.3, 34-1694 of SEQ ID No.4, 1724-3406 of SEQ ID No.4, 34-1525 of SEQ ID No.5, 34-2041 of SEQ ID No.6 and 37-1437 or 1708 of SEQ ID No.7.

16. A nucleic acid according to claim 15 comprising a sequence selected from the group consisting of bases 17147-18472, 18974-23332, 23785-28767, 28855-33903, 34284-38759, 39221-45244, 45622-49824 or 50637 of SEQ ID No.1.

17. An isolated or recombinant nucleic acid as defined in any one of the preceding claims wherein said nucleic acid sequence is selected from the group of genes consisting of: *borA1* (16184-18814 of SEQ ID NO: 1), *borA2* (18875-23590 of SEQ ID NO: 1), *borA3* (23686-34188 of SEQ ID NO: 1), *borA4* (34185-39047 of SEQ ID NO: 1), *borA5* (39122-45514 of SEQ ID NO: 1), *borA6* (45514-50742 of SEQ ID NO: 1), *borB* (7603-8397 of the complement strand of SEQ ID NO: 1), *borC* (8397-9194 of the complement strand of SEQ ID NO: 1), *borD* (9244-9996 of the complement strand of SEQ ID NO: 1), *borE* (9993-11165 of the complement strand of SEQ ID NO: 1), *borF* (11162-11980 of the complement strand of SEQ ID NO: 1), *borG* (11992-13611 of the complement strand of SEQ ID NO: 1), *borH* (13608-15659 of the complement strand of SEQ ID NO: 1), *borI* (50739-52019 of SEQ ID NO: 1), *borJ* (52113-53477 of SEQ ID NO: 1), *borK* (53486-54466 of SEQ ID NO: 1), *borL* (54506-56176 of SEQ ID NO: 1), *borM* (56181-57098 of SEQ ID NO: 1), *borN* (57112-57858 of SEQ ID NO: 1), *borO* (57939-59966 of SEQ ID NO: 1), *orfB1* (2-313 of SEQ ID NO: 1), *orfB2* (501-3107 of SEQ ID NO: 1), *orfB3* (3172-3810 of the complement strand of SEQ ID NO: 1), *orfB4* (3935-4924 of the complement strand of SEQ ID NO: 1), *orfB5* (5123-5953 of SEQ ID NO: 1), *orfB6* (5961-6518 of the complement strand of SEQ ID NO: 1), *orfB7* (6564-7538 of SEQ ID NO: 1), *orfB8* (60153-60533 of the complement strand of SEQ ID NO: 1), *orfB9* (60620-61003 of SEQ ID NO: 1), *orfB10* (61188-61436 of SEQ ID NO: 1),

*orfB11* (61526-61738 of SEQ ID NO: 1), *orfB12* (61767-62285 of the complement strand of SEQ ID NO: 1), *orfB13a* (62750-63067 of the complement strand of SEQ ID NO: 1), *orfB13b* (62586-62858 of the complement strand of SEQ ID NO: 1), *orfB14* (63155-65071 of the complement strand of SEQ ID NO: 1), *orfB15* (65374-65871 of SEQ ID NO: 1), *orfB16* (65942-68305 of the complement strand of SEQ ID NO:1), *orfB17* (68290-68910 of the complement strand of SEQ ID NO: 1), *orfB18* (69681-70436 of SEQ ID NO: 1), *orfB19* (70445-71848 of SEQ ID NO: 1), *orfB20* (71851-72957 of SEQ ID NO: 1), *orfB21* (73037-73942 of SEQ ID NO: 1) and *orfB22* (73995-74534 of the complement strand of SEQ ID NO: 1).

18. An isolated polypeptide encoded by the nucleic acid sequence of any one of the preceding claims.

19. A method of modifying a parent polyketide synthase, comprising introducing into a host cell a nucleic acid encoding a domain from a borrelidin polyketide synthase, or a derivative thereof, wherein the host cell contains nucleic acid encoding said parent polyketide synthase, such that, when expressed, the domain is incorporated into said parent polyketide synthase.

20. A method according to claim 19 wherein the borrelidin PKS domain is inserted in addition to the native domains of the parent PKS.

21. A method according to claim 19 wherein the borrelidin PKS domain is inserted in place of a native domain of the parent PKS.

22. A method according to claim 21 wherein a domain of the parent polyketide synthase is inactivated, deleted or altered.

23. A method according to any one of claims 19 to 22 comprising introducing a nucleic acid encoding a module from said borrelidin polyketide synthase, or a derivative thereof, into said host cell.

24. A method according to claim 23 wherein said module is an extender module comprising at least ACP, AT and KS domains.

25. A method according to claim 24 wherein said module further comprises a KR domain.

26. A method according to claim 25 wherein said module further comprises a DH domain.

27. A method according to claim 26 wherein said module further comprises an ER domain.

28. A method according to any one of claims 24 to 27 wherein said module further comprises a TE domain.

29. A method of modifying a parent borrelidin polyketide synthase comprising introducing into a host cell a nucleic acid encoding a domain from a donor polyketide synthase, wherein the host cell contains nucleic acid encoding said parent borrelidin polyketide synthase, such that, when expressed, the domain is incorporated into said parent borrelidin polyketide synthase.

30. A method according to claim 29 wherein the donor PKS domain is inserted in addition to the native domains of the parent borrelidin PKS.

31. A method according to claim 29 wherein the donor PKS domain is inserted in place of a native domain of the parent borrelidin PKS.

32. A method according to any one of claims 29 to 31 wherein the donor PKS domain is selected from the group consisting of O-methyl transferase domains, C-methyl transferase domains, epimerisation domains, monooxygenase domains, dehydrogenase domains, aminotransferase domains or non-ribosomal peptide synthetase domains.

33. A method according to any one of claims 29 to 32 comprising introducing a nucleic acid encoding a module from said donor polyketide synthase, or a derivative thereof, into said host cell.

34. A method according to claim 33 wherein said module is an extender module comprising at least ACP, AT and KS domains.

35. A method according to claim 34 wherein said module further comprises a KR domain.

36. A method according to claim 35 wherein said module further comprises a DH domain.

37. A method according to claim 36 wherein said module further comprises an ER domain.

38. A method according to any one of claims 33 to 37 wherein said module further comprises a TE domain.

39. A method according to any one of claims 29 to 31 wherein the donor PKS is a borrelidin PKS.

40. A nucleic acid construct comprising at least one first nucleic acid portion encoding at least one domain of a borrelidin PKS and a second nucleic acid portion or portions encoding at least one type I PKS domain which is heterologous to said borrelidin PKS.

41. A construct according to claim 40 comprising a hybrid polyketide synthase gene, said gene encoding at least one domain of a borrelidin PKS and at least one type I PKS domain which is heterologous to said borrelidin PKS.

42. A method for increasing the capacity of a host cell to produce borrelidin, or a borrelidin derivative or analogue in a host cell expressing a polyketide synthase, said method comprising upregulating a borrelidin biosynthetic gene involved in production of the borrelidin starter unit in said cell.

43. A method according to claim 42 wherein said gene is selected from the group consisting of *borC, borD, borE, borF, borH, borK, borL, borM and borN.*

44. A method according to claim 43 wherein the gene is *borE* or *borL.*

45. A method according to any one of claims 42 to 44 comprising the step of introducing a nucleic acid encoding the gene to be upregulated into said cell.

46. A method for modifying a host cell to increase its capacity for the production of borrelidin, or a borrelidin derivative or analogue, the host cell being capable of expressing a polyketide synthase for borrelidin or said derivative or analogue, the method comprising deleting, disrupting, or otherwise inactivating a borrelidin biosynthetic gene involved in production of the borrelidin starter unit in said cell, wherein the gene is *borG.*

47. A method according to claim 46 comprising fermenting the resulting cell and feeding an exogenous carboxylic acid.

48. The method of claim 47, wherein the exogenous carboxylic acid is selected from the group consisting of *trans*-cyclobutane-1,2-dicarboxylic acid, 2,3-dimethylsuccinic acid, 2-methylsuccinic acid, and *trans*-cyclopentane-1,2-dicarboxylic acid

49. The method of any one of claims 44 to 48, wherein the method additionally comprises deleting, modifying or replacing one or more borrelidin biosynthetic genes, or borrelidin polyketide synthase domains or modules.

50. A method for producing a modified borrelidin polyketide or derivative thereof in a host cell expressing a PKS for borrelidin or a derivative thereof, the method comprising the deletion or inactivation of the genes responsible for the formation of the nitrile function at C12 of borrelidin.

51. A method according to claim 50 comprising the introduction into said host cell of nucleic acid encoding one or more heterologous genes to allow alternative elaboration of any accumulated biosynthetic intermediates or shunt metabolites.

52. A vector which comprises a nucleic acid molecule as defined in any one of claims 1 to 17 or a construct as defined in claim 40 or claim 41.

53. A host cell comprising the vector of claim 52.

54. The host cell of claim 53, wherein the host cell is an Actinomycete.

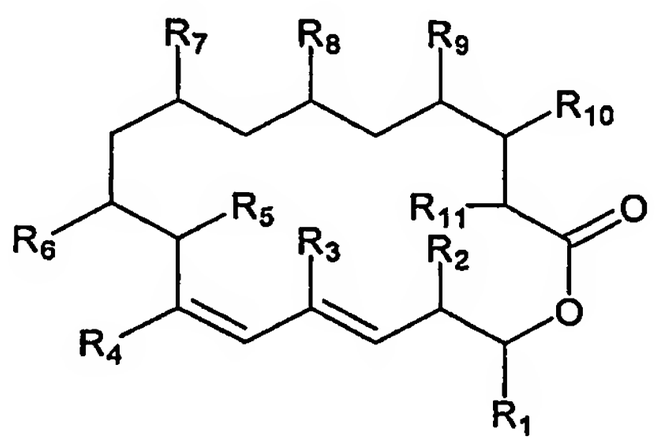
55. The host cell of claim 53, wherein the host cell is a Streptomycete.

56. The host cell of claim 55, wherein the host cell is selected from the group consisting of *Saccharopolyspora erythraea, Streptomyces coelicolor, Streptomyces avermitilis, Streptomyces griseofuscus, Streptomyces cinnamonensis, Micromonospora griseorubida, Streptomyces hygroscopicus, Streptomyces fradiae, Streptomyces longisporoflavus, Streptomyces lasaliensis, Streptomyces tsukubaensis, Streptomyces griseus, Streptomyces venezuelae, Streptomyces antibioticus, Streptomyces lividans, Streptomyces rimosus and Streptomyces albus. Streptomyces rochei* ATCC23956, *Streptomyces parvulus* Tü113.

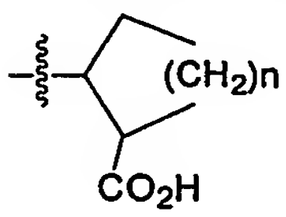
57. A method for the synthesis of polyketides comprising culturing the host cell of any one of claims 53 to 56.

58. A compound of formula 1 or a pharmaceutically acceptable salt thereof, wherein:

Formula 1



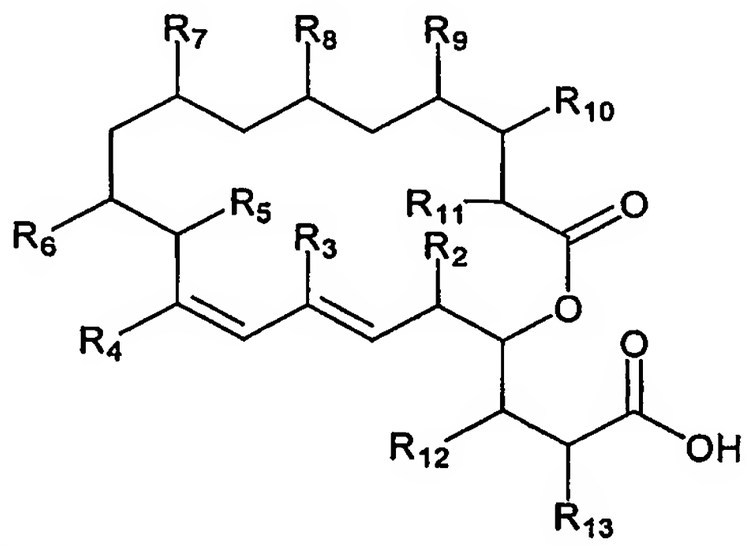
$R_1$ is a cycloalkyl group of varying size (n = 1- 2) and substituted as shown below;




wherein $R_1$ can also optionally be substituted with one or more halo atoms or one or more $C_1$ to $C_3$ alkyl groups; $R_2$, $R_3$, $R_6$, $R_7$, $R_8$, $R_9$,or $R_{11}$ are each independently H, $OCH_3$, $CH_3$ or $CH_2CH_3$; $R_4$ is CN, $CO_2H$, CHO, $CH_3$, $CONH_2$, CHNH, $R_5$, $R_{10}$ are OH; or analogues differing from the corresponding "natural" compound in the oxidation state of one or more of the ketide units (i.e. selection of alternatives from the group: -CO-, -CH(OH)-, =CH-, and –CH2-), with the proviso that said compounds are not borrelidin (**1**), 12-desnitrile-12-carboxyl borrelidin (**2**), 10-desmethyl borrelidin (**3**), 11-epiborrelidin (**4**) or C14,C15-*cis* borrelidin analogue (**5**) as shown in Figure 1.

59. A compound of formula 2 or a pharmaceutically acceptable salt thereof, wherein:

Formula 2




$R_2$, $R_3$, $R_6$, $R_7$, $R_8$, $R_9$,or $R_{11}$ are each independently H, $OCH_3$, $CH_3$ or $CH_2CH_3$; $R_4$ is CN, $CO_2H$, CHO, $CH_3$, $CONH_2$, CHNH, $R_5$, $R_{10}$ are OH; or analogues differing from the corresponding "natural" compound in the oxidation state of one or more of the ketide units (i.e. selection of alternatives from the group: -CO-, -CH(OH)-, =CH-, and $–CH_2$-), and $R_{12}$ and $R_{13}$ are independently H or a C1-C4 alkyl group which may be optionally substituted with OH, F, Cl, SH) with the proviso that $R_{12}$ and $R_{13}$ are not simultaneously H.

60. A compound or salt according to claim 58 or claim 59, wherein $R_7$, $R_8$ and $R_9$ are all $CH_3$.

61. A compound or salt according to claim 58 or claim 59, wherein $R_4$ is $CH_3$ or COOH.

62. A compound or salt according to claim 60 wherein $R_4$ is $CH_3$ or COOH.

63. A compound or salt according to claim 58 or claim 59, wherein $R_4$ is CN.

64. A compound or salt according to claim 60 wherein $R_4$ is CN.

65. A compound or salt according to claim 58 wherein R1 is cyclobutane-1'-carboxylate.

66. A compound or salt according to claim 60, wherein R1 is cyclobutane-1'-carboxylate

67. A compound or salt according to claim 66, wherein $R_4$ is $CH_3$ or COOH

68. A compound or salt according to claim 58, wherein $R_6$, $R_7$, $R_8$ and $R_9$ are all $CH_3$, $R_2$ and $R_{11}$ are H, $R_5$ and $R_{10}$ are OH, $R_4$ is either $CH_3$, COOH or CN and $R_1$ is cyclopentane-1'-carboxylate or. cyclobutane-1'-carboxylate

69. A compound or salt according to claim 59, wherein $R_{12}$ and $R_{13}$ are independently $CH_3$ or H

70. A compound or salt according to claim 60, wherein $R_{12}$ and $R_{13}$ are independently $CH_3$ or H

71. A compound or salt according to claim 70, wherein $R_4$ is $CH_3$ or COOH

72. A compound or salt according to claim 59 wherein $R_6$, $R_7$, $R_8$ and $R_9$ are all $CH_3$, $R_2$ and $R_{11}$ are H, $R_5$ and $R_{10}$ are OH, $R_4$ is either $CH_3$, COOH or CN and $R_{12}$ and $R_{13}$ are independently $CH_3$ or H

73. A compound or salt according to claim 59 wherein $R_6$, $R_7$, $R_8$ and $R_9$ are all $CH_3$, $R_2$ and $R_{11}$ are H, $R_5$ and $R_{10}$ are OH, $R_4$ is either $CH_3$, COOH or CN and $R_{12}$ and $R_{13}$ are both $CH_3$.

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